

December 21 2007--0275543 sequence listing\_ST25.txt  
SEQUENCE LISTING

<110> Hanna, Nabil  
Newman, Roland A.  
Reff, Mitchell E.

<120> Recombinant Anti-CD4 Antibodies for Human Therapy

<130> 037003-0275543

<140> 09/612,914

<141> 2000-07-10

<150> 08/523,894

<151> 1995-09-06

<150> 08/476,237

<151> 1995-06-07

<160> 59

<170> PatentIn version 3.4

<210> 1

<211> 423

<212> DNA

<213> Monkey

<220>

<221> misc\_feature

<222> (4)..(423)

<223> Heavy chain variable domain of CE9.1

<220>

<221> CDS

<222> (4)..(423)

<220>

<221> mat\_peptide

<222> (61)..(423)

<400> 1

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Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg		
				-15						-10					-5	

tgg	gtc	ttg	tcc	cag	gtg	cag	ctg	cag	gag	gcg	ggc	cca	gga	ctg	gtg	96
Trp	Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ala	Gly	Pro	Gly	Leu	Val	
		-1	1				5						10			

aag	cct	tcg	gag	acc	ctg	tcc	ctc	acc	tgc	agt	gtc	tct	ggg	ggc	tcc	144
Lys	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ser	Val	Ser	Gly	Gly	Ser	
		15					20					25				

atc	agc	ggg	gac	tat	tat	tgg	ttc	tgg	atc	cgc	cag	tcc	cca	ggg	aag	192
Ile	Ser	Gly	Asp	Tyr	Tyr	Trp	Phe	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Lys	
	30					35				40						

gga	ctg	gag	tgg	atc	ggc	tac	atc	tat	ggc	agt	ggg	ggc	acc	aat		240
Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Gly	Ser	Gly	Gly	Gly	Thr	Asn	
45					50					55					60	

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tac aat ccc tcc ctc aac aat cga gtc tcc att tca ata gac acg tcc 288  
Tyr Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser  
65 70 75

aag aac ctc ttc tcc ctg aaa ctg agg tct gtg acc gcc gcg gac acg 336  
Lys Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr  
80 85 90

gcc gtc tat tac tgt gcg agt aat ata ttg aaa tat ctt cac tgg tta 384  
Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu  
95 100 105

tta tac tgg ggc cag gga gtc ctg gtc acc gtc tcc tca 423  
Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
110 115 120

<210> 2  
<211> 140  
<212> PRT  
<213> Monkey

<400> 2

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
-15 -10 -5

Val Leu Ser Gln Val Gln Leu Gln Glu Ala Gly Pro Gly Leu Val Lys  
-1 1 5 10

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile  
15 20 25

Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly  
30 35 40 45

Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr  
50 55 60

Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys  
65 70 75

Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala  
80 85 90

Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu  
95 100 105

Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
110 115 120

<210> 3  
<211> 387  
<212> DNA

&lt;213&gt; Monkey

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (4)..(387)

&lt;223&gt; Light chain variable domain of CD9.1

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (4)..(387)

&lt;220&gt;

&lt;221&gt; mat\_peptide

&lt;222&gt; (61)..(387)

&lt;400&gt; 3

acc atg gcc tgg gct ctg ctg ctc ctc ggc ctc ctt gct cac ttt aca 48  
 Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Ala His Phe Thr  
 -15 -10 -5

gac tct gcg gcc tcc tat gag ttg agt cag cct cgc tca gtg tcc gtg 96  
 Asp Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val  
 -1 1 5 10

tcc cca gga cag acg gcc ggg ttc acc tgt ggg gga gac aac gtt gga 144  
 Ser Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly  
 15 20 25

agg aaa agt gta cag tgg tac cag cag aag cca ccg cag gcc cct gtg 192  
 Arg Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val  
 30 35 40

ctg gtc atc tat gct gac agc gaa cgg ccc tca ggg atc cct gcg cga 240  
 Leu Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg  
 45 50 55 60

ttc tct ggc tcc aac tca ggg aac acc gcc acc ctg acc atc agc ggg 288  
 Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly  
 65 70 75

gtc gag gcc ggg gat gag gct gac tat tac tgt cag gtg tgg gac agt 336  
 Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser  
 80 85 90

act gct gat cat tgg gtc ttc ggc gga ggg acc cgg ctg acc gtc cta 384  
 Thr Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu  
 95 100 105

ggt 387  
 Gly

&lt;210&gt; 4

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Monkey

&lt;400&gt; 4

Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp  
 -15 -10 -5

Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser  
-1 1 5 10

Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly Arg  
15 20 25

Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val Leu  
30 35 40 45

Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg Phe  
50 55 60

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val  
65 70 75

Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Thr  
80 85 90

Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly  
95 100 105

<210> 5  
<211> 702  
<212> DNA  
<213> Human or Monkey

<220>  
<221> misc\_feature  
<222> (1)..(702)  
<223> Lambda variable and constant domains in CE9.1

<220>  
<221> CDS  
<222> (1)..(702)

<400> 5  
atg gcc tgg gct ctg ctg ctc ctc ggc ctc ctt gct cac ttt aca gac 48  
Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp  
1 5 10 15

tct gcg gcc tcc tat gag ttg agt cag cct cgc tca gtg tcc gtg tcc 96  
Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser  
20 25 30

cca gga cag acg gcc ggg ttc acc tgt ggg gga gac aac gtt gga agg 144  
Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly Arg  
35 40 45

aaa agt gta cag tgg tac cag cag aag cca ccg cag gcc cct gtg ctg 192  
Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val Leu  
50 55 60

gtc atc tat gct gac agc gaa cgg ccc tca ggg atc cct gcg cga ttc 240  
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Val	Ile	Tyr	Ala	Asp	Ser	Glu	Arg	Pro	Ser	Gly	Ile	Pro	Ala	Arg	Phe		
65					70					75					80		
tct	ggc	tcc	aac	tca	ggg	aac	acc	gcc	acc	ctg	acc	atc	agc	ggg	gtc	288	
Ser	Gly	Ser	Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Val		
				85					90					95			
gag	gcc	ggg	gat	gag	gct	gac	tat	tac	tgt	cag	gtg	tgg	gac	agt	act	336	
Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Ser	Thr		
			100					105					110				
gct	gat	cat	tgg	gtc	ttc	ggc	gga	ggg	acc	cgg	ctg	acc	gtc	cta	ggt	384	
Ala	Asp	His	Trp	Val	Phe	Gly	Gly	Gly	Thr	Arg	Leu	Thr	Val	Leu	Gly		
		115					120					125					
cag	ccc	aag	gct	gcc	ccc	tcg	gtc	act	ctg	ttc	ccg	ccc	tcc	tct	gag	432	
Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	Glu		
	130					135					140						
gag	ctt	caa	gcc	aac	aag	gcc	aca	ctg	gtg	tgt	ctc	ata	agt	gac	ttc	480	
Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	Phe		
	145				150					155					160		
tac	ccg	gga	gcc	gtg	aca	gtg	gcc	tgg	aag	gca	gat	agc	agc	ccc	gtc	528	
Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	Val		
				165				170						175			
aag	gcg	gga	gtg	gag	acc	acc	aca	ccc	tcc	aaa	caa	agc	aac	aac	aag	576	
Lys	Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	Lys		
			180					185					190				
tac	gcg	gcc	agc	agc	tac	ctg	agc	ctg	acg	cct	gag	cag	tgg	aag	tcc	624	
Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	Ser		
		195					200					205					
cac	aga	agc	tac	agc	tgc	cag	gtc	acg	cat	gaa	ggg	agc	acc	gtg	gag	672	
His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	Glu		
	210					215					220						
aag	aca	gtg	gcc	cct	aca	gaa	tgt	tca	tga							702	
Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser									
	225				230												

<210> 6  
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 <212> PRT  
 <213> Human or Monkey

<400> 6

Met	Ala	Trp	Ala	Leu	Leu	Leu	Leu	Gly	Leu	Leu	Ala	His	Phe	Thr	Asp		
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Ser	Ala	Ala	Ser	Tyr	Glu	Leu	Ser	Gln	Pro	Arg	Ser	Val	Ser	Val	Ser		
			20					25				30					
Pro	Gly	Gln	Thr	Ala	Gly	Phe	Thr	Cys	Gly	Gly	Asp	Asn	Val	Gly	Arg		
	35						40					45					

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Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val Leu
 50          55          60

Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg Phe
 65          70          75          80

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val
          85          90          95

Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Thr
          100          105          110

Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly
          115          120          125

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
          130          135          140

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
          145          150          155          160

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
          165          170          175

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
          180          185          190

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
          195          200          205

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
          210          215          220

Lys Thr Val Ala Pro Thr Glu Cys Ser
          225          230

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<210> 7
<211> 1404
<212> DNA
<213> Human or Monkey

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<220>
<221> misc_feature
<222> (1)..(1404)
<223> Heavy chain variable and constant gamma 4

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<220>
<221> CDS
<222> (1)..(1404)

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<400> 7
atg aaa cac ctg tgg ttc ttc ctc ctc ctg gtg gca gcc ccc aga tgg      48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1      5      10      15

gtc ttg tcc cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag      96
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
20      25      30

cct tcg gag acc ctg tcc ctc acc tgc agt gtc tct ggt ggc tcc atc     144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile
35      40      45

agc ggt gac tat tat tgg ttc tgg atc cgc cag tcc cca ggg aag gga     192
Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly
50      55      60

ctg gag tgg atc ggc tac atc tat ggc agt ggt ggg ggc acc aat tac     240
Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr
65      70      75

aat ccc tcc ctc aac aat cga gtc tcc att tca ata gac acg tcc aag     288
Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys
85      90      95

aac ctc ttc tcc ctg aaa ctg agg tct gtg acc gcc gcg gac acg gcc     336
Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala
100     105     110

gtc tat tac tgt gcg agt aat ata ttg aaa tat ctt cac tgg tta tta     384
Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu
115     120     125

tac tgg ggc cag gga gtc ctg gtc acc gtc tcc tca gct agc acc aag     432
Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys
130     135     140

ggc cca tcc gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag     480
Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
145     150     155

agc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg     528
Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165     170     175

gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc     576
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180     185     190

ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg     624
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195     200     205

gtg acc gtg ccc tcc agc agc ttg ggc acg aag acc tac acc tgc aac     672
Val Thr Val Pro Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn
210     215     220

gta gat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag tcc     720
Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser
225     230     235

aaa tat ggt ccc cca tgc cca tca tgc cca gca cct gag ttc ctg ggg     768
Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly

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gga cca tca gtc ttc ctg ttc ccc cca aaa ccc aag gac act ctc atg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 260 265 270	816
atc tcc cgg acc cct gag gtc acg tgc gtg gtg gtg gac gtg agc cag Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln 275 280 285	864
gaa gac ccc gag gtc cag ttc aac tgg tac gtg gat ggc gtg gag gtg Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val 290 295 300	912
cat aat gcc aag aca aag ccg cgg gag gag cag ttc aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr 305 310 315 320	960
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aac ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335	1008
aag gag tac aag tgc aag gtc tcc aac aaa ggc ctc ccg tcc tcc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile 340 345 350	1056
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gag cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365	1104
tac acc ctg ccc cca tcc cag gag gag atg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser 370 375 380	1152
ctg acc tgc ctg gtc aaa ggc ttc tac ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400	1200
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 405 410 415	1248
gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc agg cta acc gtg Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val 420 425 430	1296
gac aag agc agg tgg cag gag ggg aat gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445	1344
cat gag gct ctg cac aac cac tac aca cag aag agc ctc tcc ctg tct His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460	1392
ctg ggt aaa tga Leu Gly Lys 465	1404

<210> 8  
<211> 467  
<212> PRT  
<213> Human or Monkey



<400> 8

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys  
20 25 30

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile  
35 40 45

Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly  
50 55 60

Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr  
65 70 75 80

Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys  
85 90 95

Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala  
100 105 110

Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu  
115 120 125

Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
145 150 155 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn  
210 215 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser  
225 230 235 240

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Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly  
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
275 280 285

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile  
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
355 360 365

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser  
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val  
420 425 430

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met  
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
450 455 460

Leu Gly Lys  
465

<210> 9  
<211> 1404  
<212> DNA

&lt;213&gt; Human or Monkey

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1404)

&lt;223&gt; Heavy chain gamma 4 with the E mutation

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1404)

&lt;400&gt; 9

atg	aaa	cac	ctg	tgg	ttc	ttc	ctc	ctc	ctg	gtg	gca	gcc	ccc	aga	tgg	48
Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp	
1				5					10					15		

gtc	ttg	tcc	cag	gtg	cag	ctg	cag	gag	tcg	ggc	cca	gga	ctg	gtg	aag	96
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	
			20					25					30			

cct	tcg	gag	acc	ctg	tcc	ctc	acc	tgc	agt	gtc	tct	ggg	ggc	tcc	atc	144
Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ser	Val	Ser	Gly	Gly	Ser	Ile	
		35					40					45				

agc	ggg	gac	tat	tat	tgg	ttc	tgg	atc	cgc	cag	tcc	cca	ggg	aag	gga	192
Ser	Gly	Asp	Tyr	Tyr	Trp	Phe	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Lys	Gly	
	50					55					60					

ctg	gag	tgg	atc	ggc	tac	atc	tat	ggc	agt	ggg	ggg	ggc	acc	aat	tac	240
Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Gly	Ser	Gly	Gly	Gly	Thr	Asn	Tyr	
65				70				75						80		

aat	ccc	tcc	ctc	aac	aat	cga	gtc	tcc	att	tca	ata	gac	acg	tcc	aag	288
Asn	Pro	Ser	Leu	Asn	Asn	Arg	Val	Ser	Ile	Ser	Ile	Asp	Thr	Ser	Lys	
				85				90						95		

aac	ctc	ttc	tcc	ctg	aaa	ctg	agg	tct	gtg	acc	gcc	gcg	gac	acg	gcc	336
Asn	Leu	Phe	Ser	Leu	Lys	Leu	Arg	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	
			100					105					110			

gtc	tat	tac	tgt	gcg	agt	aat	ata	ttg	aaa	tat	ctt	cac	tgg	tta	tta	384
Val	Tyr	Tyr	Cys	Ala	Ser	Asn	Ile	Leu	Lys	Tyr	Leu	His	Trp	Leu	Leu	
		115					120					125				

tac	tgg	ggc	cag	gga	gtc	ctg	gtc	acc	gtc	tcc	tca	gct	agc	acc	aag	432
Tyr	Trp	Gly	Gln	Gly	Val	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	
	130					135					140					

ggg	cca	tcc	gtc	ttc	ccc	ctg	gcg	ccc	tgc	tcc	agg	agc	acc	tcc	gag	480
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	
145				150					155						160	

agc	aca	gcc	gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	528
Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	
				165					170					175		

gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	576
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	
			180					185					190			

ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	624
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	

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195	200	205	
gtg acc gtg ccc tcc agc agc ttg ggc acg aag acc tac acc tgc aac Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn 210 215 220			672
gta gat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag tcc Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser 225 230 235 240			720
aaa tat ggt ccc cca tgc cca tca tgc cca gca cct gag ttc gag ggg Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Glu Gly 245 250 255			768
gga cca tca gtc ttc ctg ttc ccc cca aaa ccc aag gac act ctc atg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 260 265 270			816
atc tcc cgg acc cct gag gtc acg tgc gtg gtg gtg gac gtg agc cag Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln 275 280 285			864
gaa gac ccc gag gtc cag ttc aac tgg tac gtg gat ggc gtg gag gtg Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val 290 295 300			912
cat aat gcc aag aca aag ccg cgg gag gag cag ttc aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr 305 310 315 320			960
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aac ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335			1008
aag gag tac aag tgc aag gtc tcc aac aaa ggc ctc ccg tcc tcc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile 340 345 350			1056
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gag cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365			1104
tac acc ctg ccc cca tcc cag gag gag atg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser 370 375 380			1152
ctg acc tgc ctg gtc aaa ggc ttc tac ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400			1200
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 405 410 415			1248
gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc agg cta acc gtg Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val 420 425 430			1296
gac aag agc agg tgg cag gag ggg aat gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445			1344
cat gag gct ctg cac aac cac tac aca cag aag agc ctc tcc ctg tct			1392

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
450 455 460

ctg ggt aaa tga  
Leu Gly Lys  
465

1404

<210> 10  
<211> 467  
<212> PRT  
<213> Human or Monkey  
  
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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys  
20 25 30

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile  
35 40 45

Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly  
50 55 60

Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr  
65 70 75 80

Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys  
85 90 95

Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala  
100 105 110

Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu  
115 120 125

Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
145 150 155 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
 195 200 205  
 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn  
 210 215 220  
 Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser  
 225 230 235 240  
 Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Glu Gly  
 245 250 255  
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 260 265 270  
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
 275 280 285  
 Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 290 295 300  
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
 305 310 315 320  
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 325 330 335  
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile  
 340 345 350  
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 355 360 365  
 Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser  
 370 375 380  
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 385 390 395 400  
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 405 410 415  
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val  
 420 425 430  
 Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met  
 435 440 445

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His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
450 455 460

Leu Gly Lys  
465

<210> 11  
<211> 1404  
<212> DNA  
<213> Human or Monkey

<220>  
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<222> (1)..(1404)  
<223> Heavy chain gamma 4 with the P and E mutation

<220>  
<221> CDS  
<222> (1)..(1404)

<400> 11  
atg aaa cac ctg tgg ttc ttc ctc ctc ctg gtg gca gcc ccc aga tgg 48  
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
1 5 10 15  
gtc ttg tcc cag gtg cag ctg cag gag tgc ggc cca gga ctg gtg aag 96  
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys  
20 25 30  
cct tgc gag acc ctg tcc ctc acc tgc agt gtc tct ggt ggc tcc atc 144  
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile  
35 40 45  
agc ggt gac tat tat tgg ttc tgg atc cgc cag tcc cca ggg aag gga 192  
Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly  
50 55 60  
ctg gag tgg atc ggc tac atc tat ggc agt ggt ggg ggc acc aat tac 240  
Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr  
65 70 75 80  
aat ccc tcc ctc aac aat cga gtc tcc att tca ata gac acg tcc aag 288  
Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys  
85 90 95  
aac ctc ttc tcc ctg aaa ctg agg tct gtg acc gcc gcg gac acg gcc 336  
Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala  
100 105 110  
gtc tat tac tgt gcg agt aat ata ttg aaa tat ctt cac tgg tta tta 384  
Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu  
115 120 125  
tac tgg ggc cag gga gtc ctg gtc acc gtc tcc tca gct agc acc aag 432  
Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
130 135 140  
ggg cca tcc gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag 480  
Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
145 150

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145	150	155	160	
agc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg				528
Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro	165	170	175	
gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc				576
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr	180	185	190	
ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg				624
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val	195	200	205	
gtg acc gtg ccc tcc agc agc ttg ggc acg aag acc tac acc tgc aac				672
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn	210	215	220	
gta gat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag tcc				720
Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser	225	230	235	240
aaa tat ggt ccc cca tgc cca cca tgc cca gca cct gag ttc gag ggg				768
Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly	245	250	255	
gga cca tca gtc ttc ctg ttc ccc cca aaa ccc aag gac act ctc atg				816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met	260	265	270	
atc tcc cgg acc cct gag gtc acg tgc gtg gtg gtg gac gtg agc cag				864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln	275	280	285	
gaa gac ccc gag gtc cag ttc aac tgg tac gtg gat ggc gtg gag gtg				912
Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val	290	295	300	
cat aat gcc aag aca aag ccg cgg gag gag cag ttc aac agc acg tac				960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr	305	310	315	320
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aac ggc				1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly	325	330	335	
aag gag tac aag tgc aag gtc tcc aac aaa ggc ctc ccg tcc tcc atc				1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile	340	345	350	
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gag cca cag gtg				1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val	355	360	365	
tac acc ctg ccc cca tcc cag gag gag atg acc aag aac cag gtc agc				1152
Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser	370	375	380	
ctg acc tgc ctg gtc aaa ggc ttc tac ccc agc gac atc gcc gtg gag				1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu	385	390	395	400
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc				1248



Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro		
				405					410					415			
gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	agg	cta	acc	gtg		1296
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val		
			420					425					430				
gac	aag	agc	agg	tgg	cag	gag	ggg	aat	gtc	ttc	tca	tgc	tcc	gtg	atg		1344
Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met		
			435				440					445					
cat	gag	gct	ctg	cac	aac	cac	tac	aca	cag	aag	agc	ctc	tcc	ctg	tct		1392
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser		
			450			455					460						
ctg	ggt	aaa	tga														1404
Leu	Gly	Lys															
			465														

<210> 12  
 <211> 467  
 <212> PRT  
 <213> Human or Monkey  
 <400> 12

Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp		
1				5					10					15			
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys		
			20					25					30				
Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ser	Val	Ser	Gly	Gly	Ser	Ile		
			35				40					45					
Ser	Gly	Asp	Tyr	Tyr	Trp	Phe	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Lys	Gly		
		50				55					60						
Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Gly	Ser	Gly	Gly	Gly	Thr	Asn	Tyr		
					70					75					80		
Asn	Pro	Ser	Leu	Asn	Asn	Arg	Val	Ser	Ile	Ser	Ile	Asp	Thr	Ser	Lys		
				85					90					95			
Asn	Leu	Phe	Ser	Leu	Lys	Leu	Arg	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala		
			100					105					110				
Val	Tyr	Tyr	Cys	Ala	Ser	Asn	Ile	Leu	Lys	Tyr	Leu	His	Trp	Leu	Leu		
			115				120					125					
Tyr	Trp	Gly	Gln	Gly	Val	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys		
						135					140						

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
145 150 155 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn  
210 215 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser  
225 230 235 240

Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly  
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
275 280 285

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile  
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
355 360 365

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser  
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val  
420 425 430

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met  
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
450 455 460

Leu Gly Lys  
465

<210> 13  
<211> 26  
<212> DNA  
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<220>  
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<222> (1)..(26)  
<223> VH1 leader sequence

<400> 13  
actaagtcga catggactgg acctgg

26

<210> 14  
<211> 31  
<212> DNA  
<213> Human or Monkey

<220>  
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<222> (1)..(31)  
<223> VH2 leader sequence

<400> 14  
actaagtcga catggacata ctttgttcca c

31

<210> 15  
<211> 29  
<212> DNA  
<213> Human or Monkey

<220>  
<221> misc\_feature  
<222> (1)..(29)  
<223> VH3 leader sequence

<400> 15

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actaagtcga catggagttt gggctgagc

<210> 16  
<211> 31  
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<223> VH4 leader sequence

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<210> 17  
<211> 31  
<212> DNA  
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<220>  
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<222> (1)..(31)  
<223> VH5 leader sequence

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<210> 18  
<211> 31  
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<222> (1)..(31)  
<223> VH6 leader sequence

<400> 18  
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<210> 19  
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<220>  
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<400> 19  
ggcagcagcn acgcgtgccc actccgaggt 30

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<211> 30  
<212> DNA  
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<223> VH2 leader sequence with MluI site

<220>  
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<223> n is T or C

<400> 20  
gaccgtcccg acgcgtgtnt tgtcccaggt 30

<210> 21  
<211> 27  
<212> DNA  
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<220>  
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gctattttca cgcgtgtcca gtgtgag 27

<210> 22  
<211> 27  
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<220>  
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<223> VH4 leader sequence with MluI site

<400> 22  
gcggctccca cgcgtgtcct gtcccag 27

<210> 23  
<211> 30  
<212> DNA  
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<220>  
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<222> (1)..(30)
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<400> 23
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<210> 24
<211> 23
<212> DNA
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<220>
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<222> (1)..(23)
<223> VH1, 3a 5 primer with Xho I site

<400> 24
caggtgcagc tgctcgagtc tgg 23

<210> 25
<211> 23
<212> DNA
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<220>
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<222> (1)..(23)
<223> VH2 primer with Xho I site

<400> 25
caggtcaact tactcgagtc tgg 23

<210> 26
<211> 23
<212> DNA
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<220>
<221> misc_feature
<222> (1)..(23)
<223> VH3b primer with XhoI site

<400> 26
gaggtgcagc tgctcgagtc tgg 23

<210> 27
<211> 23
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<220>
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<223> VH4 primer with XhoI site

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<400> 27  
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<210> 28  
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<220>  
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<223> VH6 primer with XhoI site

<400> 28  
caggtacagc tgctcgagtc agg 23

<210> 29  
<211> 26  
<212> DNA  
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<220>  
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<400> 29  
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<210> 30  
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<400> 30  
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<210> 31  
<211> 37  
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<220>  
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<223> n is G or A

<220>

<221> misc\_feature

<222> (24)..(24)

<223> n is A or T

<220>

<221> misc\_feature

<222> (29)..(29)

<223> n is T or A

<220>

<221> misc\_feature

<222> (32)..(32)

<223> n is T or G

<400> 31

atcacagatc tctcaccatg gngnccccwg cncagct

37

<210> 32

<211> 41

<212> DNA

<213> Human or Monkey

<220>

<221> misc\_feature

<222> (1)..(41)

<223> Kappa light chain primer with Bgl II site

<400> 32

atcacagatc tctcaccatg gacatgaggg tccccgctca g

41

<210> 33

<211> 41

<212> DNA

<213> Human or Monkey

<220>

<221> misc\_feature

<222> (1)..(41)

<223> Kappa light chain primer with Bgl II site.

<220>

<221> misc\_feature

<222> (26)..(26)

<223> n is G, A or C

<400> 33

atcacagatc tctcaccatg gacacnaggg cccccactca g

41

<210> 34

<211> 39

<212> DNA

<213> Human or Monkey

<220>



<221> misc\_feature  
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 <223> Lambda light chain primer with Bgl II site  
 <400> 34  
 atcacagatc tctcaccatg gcctgggctc tgctgctcc 39

<210> 35  
 <211> 39  
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 <400> 35  
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<210> 36  
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 atcacagatc tctcaccatg acctgctccc ctctcctcc 39

<210> 37  
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<220>  
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 <223> Lambda light chain primer with Bgl II site

<400> 38  
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<210> 39  
<211> 36  
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<220>  
<221> misc\_feature  
<222> (1)..(36)  
<223> Kappa light chain primer with kpn1 and BsiW1 sites

<400> 39  
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<210> 40  
<211> 30  
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<220>  
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<222> (1)..(30)  
<223> Kappa light chain primer with kpn1 and BsiW1 sites

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<210> 41  
<211> 30  
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<220>  
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<223> Lambda light chain primer with HindIII andKpn1 sites

<400> 41  
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<210> 42  
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<223> Lambda light chain primer with KpnI site

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<222> (15)..(16)  
<223> n is C or G

<400> 42  
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36

<210> 43  
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<220>  
<221> misc\_feature  
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<223> Lambda light chain primer with AvrII site

<400> 43  
cttgggctga cctaggacgg tcagccg

27

<210> 44  
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<223> VH1 heavy chain variable region

<400> 44  
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17

<210> 45  
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<223> VH2 heavy chain variable region

<400> 45  
atggacatac tttgttccac

20

<210> 46  
<211> 20  
<212> DNA  
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<220>  
<221> misc\_feature  
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<223> VH3 heavy chain variable region

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<400> 46  
ccatggagtt tgggctgagc 20

<210> 47  
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atgaaacacc tgtggttctt 20

<210> 48  
<211> 20  
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<223> VH5 heavy chain variable region

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<210> 49  
<211> 20  
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<223> VH6 heavy chain variable region

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<210> 50  
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<220>  
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<223> IgM heavy chain constant region.

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<210> 51  
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 <212> DNA  
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<220>  
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 <223> IgG1 4 heavy chain constant region

<400> 51  
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17

<210> 52  
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 <223> n is G or T

<400> 52  
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21

<210> 53  
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 <222> (5)..(5)  
 <223> n is C or T

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 <223> n is T or C

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 <222> (8)..(8)  
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<220>

<221> misc\_feature

<222> (13)..(13)

<223> n is A or C

<400> 53

ctcantnnct gcncagggtc c

21

<210> 54

<211> 19

<212> DNA

<213> Human or Monkey

<220>

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<222> (1)..(19)

<223> Kappa light chain constant region

<400> 54

aagacagatg gtgcagcca

19

<210> 55

<211> 20

<212> DNA

<213> Human or Monkey

<220>

<221> misc\_feature

<222> (1)..(20)

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<210> 56

<211> 30

<212> DNA

<213> Human or Monkey

<220>

<221> misc\_feature

<222> (1)..(30)

<223> PCR primer for Human gamma 4 constant region

<400> 56

gggggggatcc tcatttaccc agagacaggg

30

<210> 57

<211> 31

<212> DNA

<213> Human or Monkey

<220>

<221> misc\_feature

<222> (1)..(31)

<223> PCR primer for Human gamma 4 constant region

<400> 57  
gggggctagc accaagggcc catccgtctt c 31

<210> 58  
<211> 96  
<212> DNA  
<213> Human or Monkey

<220>  
<221> misc\_feature  
<222> (1)..(96)  
<223> PCR mutagenesis of human gamma 4

<400> 58  
ccgggagatc atgagagtgt ccttgggttt tggggggaac aggaagactg atggtcccc 60  
ctcgaactca ggtgctgggc atggtgggca tggggg 96

<210> 59  
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<212> DNA  
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<220>  
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<222> (1)..(27)  
<223> PCR mutagenesis of human gamma 4

<400> 59  
tcctcagcta gcaccaaggg gccatcc 27